

## SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.  
 Hannah, L. Curtis  
 Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<150> US 60/496,188  
 <151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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 <213> zea mays

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      35      40      45
Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
      50      55      60
Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
      65      70      75      80
Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
      85      90      95
Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
      100     105     110
Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
      115     120     125
Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
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Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
      145     150     155     160
Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
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Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
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 225 230 235 240  
 Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile  
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 Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe  
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 Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser  
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 Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val  
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20          25          30

Asp  Ser  Thr  Cys  Leu  Asn  Pro  Gln  Ala  His  Asp  Ser  Val  Leu  Gly  Ile
35          40          45

Ile  Leu  Gly  Gly  Gly  Ala  Gly  Thr  Arg  Leu  Tyr  Pro  Leu  Thr  Lys  Lys
50          55          60

Arg  Ala  Lys  Pro  Ala  Val  Pro  Leu  Gly  Ala  Asn  Tyr  Arg  Leu  Ile  Asp
65          70          75          80

Ile  Pro  Val  Ser  Asn  Cys  Leu  Asn  Ser  Asn  Ile  Ser  Lys  Ile  Tyr  Val
85          90          95

Leu  Thr  Gln  Phe  Asn  Ser  Ala  Ser  Leu  Asn  Arg  His  Leu  Ser  Arg  Ala
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Tyr  Gly  Ser  Asn  Ile  Gly  Gly  Tyr  Lys  Asn  Glu  Gly  Phe  Val  Glu  Val
115         120         125

Leu  Ala  Ala  Gln  Gln  Ser  Pro  Asp  Asn  Pro  Asn  Trp  Phe  Gln  Gly  Thr
130         135         140

Ala  Asp  Ala  Val  Arg  Gln  Tyr  Leu  Trp  Leu  Phe  Glu  Glu  His  Asn  Val
145         150         155         160

Met  Glu  Phe  Leu  Ile  Leu  Ala  Gly  Asp  His  Leu  Tyr  Arg  Met  Asp  Tyr
165         170         175

Glu  Lys  Phe  Ile  Gln  Ala  His  Arg  Glu  Thr  Asn  Ala  Asp  Ile  Thr  Val
180         185         190

Ala  Ala  Leu  Pro  Met  Asp  Glu  Lys  Arg  Ala  Thr  Ala  Phe  Gly  Leu  Met
195         200         205

Lys  Ile  Asp  Glu  Glu  Gly  Arg  Ile  Ile  Glu  Phe  Ala  Glu  Lys  Pro  Lys
210         215         220

Gly  Glu  Gln  Leu  Lys  Ala  Met  Met  Val  Asp  Thr  Thr  Ile  Leu  Gly  Leu
225         230         235         240

Asp  Asp  Val  Arg  Ala  Lys  Glu  Met  Pro  Tyr  Ile  Ala  Ser  Met  Gly  Ile
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Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
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Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
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Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
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Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
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Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
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Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
    385                                390                                395                                400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
    405                                410                                415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
    420                                425                                430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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          20          25          30

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Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys

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Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr
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Val	Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg
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Ala	Tyr	Gly	Ser	Asn	Ile	Gly	Gly	Tyr	Lys	Asn	Glu	Gly	Phe	Val	Glu
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Val	Leu	Ala	Ala	Gln	Gln	Ser	Pro	Asp	Asn	Pro	Asn	Trp	Phe	Gln	Gly
						135					140				
Thr	Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	Leu	Phe	Glu	Glu	His	Asn
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Tyr	Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asn	Ala	Asp	Ile	Thr
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Val	Ala	Ala	Leu	Pro	Met	Asp	Glu	Lys	Arg	Ala	Thr	Ala	Phe	Gly	Leu
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Met	Lys	Ile	Asp	Glu	Glu	Gly	Arg	Ile	Ile	Glu	Phe	Ala	Glu	Lys	Pro
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Lys	Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu	Gly
225					230					235				240	
Leu	Asp	Asp	Val	Arg	Ala	Lys	Glu	Met	Pro	Tyr	Ile	Ala	Ser	Met	Gly
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Ile	Tyr	Val	Phe	Ser	Lys	Asp	Val	Met	Leu	Gln	Leu	Leu	Arg	Glu	Gln
			260					265					270		
Phe	Pro	Glu	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala	Thr
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Ser	Ile	Gly	Lys	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu
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Asp	Ile	Gly	Thr	Ile	Ala	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	Thr
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Lys	Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Phe	Ala	Pro	Ile
			325						330					335	
Tyr	Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala	Asp
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Val	Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	Lys	Asn	Cys	Lys



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Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385              390              395              400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
405              410              415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
420              425              430

Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
435              440              445

Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
450              455              460

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465              470              475

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<211> 476
<212> PRT
<213> zea mays

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<400> 8

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
      20      25      30
Asp Ser Gln Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
      35      40      45
Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
      50      55      60
Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
      65      70      75      80
Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
      85      90      95
Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
      100      105      110
Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
      115      120      125
Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
      130      135      140
Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn

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145	150	155	160
Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp	165	170	175
Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr	180	185	190
Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu	195	200	205
Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro	210	215	220
Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly	225	230	235
Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly	245	250	255
Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln	260	265	270
Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr	275	280	285
Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu	290	295	300
Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr	305	310	315
Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile	325	330	335
Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp	340	345	350
Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys	355	360	365
Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala	370	375	380
Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu	385	390	395
Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile	405	410	415
Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg	420	425	430
Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala	435	440	445
Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val			

450	455	460	
Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile			
465	470	475	
<p>&lt;210&gt; 9            &lt;211&gt; 1428            &lt;212&gt; DNA            &lt;213&gt; zea mays</p>			
<p>&lt;400&gt; 9</p>			
atggacatgg ctttggcgctc taaagcctcc cctccgccat ggaatgccac cgcgcgcgag			60
cagccaattc caaagcgtga caaagccgct gcaaagtatt caagarcattg yctcaatcct			120
caagctcatg atagtgttct tggaatcatt ctgggaggtg gtgctgggac tagattgtac			180
cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaaacta tagactgatt			240
gataattctg tcagcaattg tctcaacagc aacatatcca agatctatgt gctaacgcaa			300
tttaactctg cttccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggaggg			360
tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccgaa taatccaaac			420
tggtttcagg gtactgcaga tgctgtaagg cagtacttgt ggttgtttga ggagcataat			480
gtgatggaat ttctaatctt tgctggcgat cacctgtacc ggatggacta tgaaaagtgc			540
attcaggcac acagagaaac aaatgctgat attaccgttg ctgccctacc gatggatgag			600
aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aagggaggat cattgagttt			660
gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc			720
cttgatgacg tgaggggcaa ggaaatgcct tatattgcta gcattgggtat ctatgttttc			780
agcaaaagtg taatgcttca gctcctccgt gaacaatttc ctgaagccaa tgactttgga			840
agtgaggtta ttccagggtc aaccagcatt ggaaagaggg ttcaggctta tctgtatgat			900
ggttactggg aagatatcgg taccattgcg gcattttata atgcgaaactt gggaataacc			960
aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaaact			1020
cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtggt tattggtgaa			1080
ggatgtgtta ttaaaaactg caagataaac cattctgtag ttggactccg atcttgcata			1140
tctgaaggtg ctatcataga ggacagtta ctaatgggtg cggactacta tgagacagaa			1200
gctgataaaa aactccttgc cgaaaaaggt ggcatctcta ttggtatttg gaaaaattca			1260
tgcatcagga gagcaatcat tgacaagaat gctcgaattg gagacaatgt taagatactc			1320
aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaagggtga			1380

attgtcacag tgatcaagga tgctttactc cctagtggaa cagttata

1428

<210> 10  
 <211> 476  
 <212> PRT  
 <213> zea mays

<400> 10

Met	Asp	Met	Ala	Leu	Ala	Ser	Lys	Ala	Ser	Pro	Pro	Pro	Trp	Asn	Ala	1	5	10	15
Thr	Ala	Ala	Glu	Gln	Pro	Ile	Pro	Lys	Arg	Asp	Lys	Ala	Ala	Ala	Asn	20	25	30	
Asp	Ser	Glu	Thr	Cys	Leu	Asn	Pro	Gln	Ala	His	Asp	Ser	Val	Leu	Gly	35	40	45	
Ile	Ile	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys	50	55	60	
Lys	Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	Ile	65	70	75	80
Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr	85	90	95	
Val	Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg	100	105	110	
Ala	Tyr	Gly	Ser	Asn	Ile	Gly	Gly	Tyr	Lys	Asn	Glu	Gly	Phe	Val	Glu	115	120	125	
Val	Leu	Ala	Ala	Gln	Gln	Ser	Pro	Asp	Asn	Pro	Asn	Trp	Phe	Gln	Gly	130	135	140	
Thr	Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	Leu	Phe	Glu	Glu	His	Asn	145	150	155	160
Val	Met	Glu	Phe	Leu	Ile	Leu	Ala	Gly	Asp	His	Leu	Tyr	Arg	Met	Asp	165	170	175	
Tyr	Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asn	Ala	Asp	Ile	Thr	180	185	190	
Val	Ala	Ala	Leu	Pro	Met	Asp	Glu	Lys	Arg	Ala	Thr	Ala	Phe	Gly	Leu	195	200	205	
Met	Lys	Ile	Asp	Glu	Glu	Gly	Arg	Ile	Ile	Glu	Phe	Ala	Glu	Lys	Pro	210	215	220	
Lys	Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu	Gly	225	230	235	240
Leu	Asp	Asp	Val	Arg	Ala	Lys	Glu	Met	Pro	Tyr	Ile	Ala	Ser	Met	Gly				

245										250										255																																		
Ile	Tyr	Val	Phe	Ser	Lys	Asp	Val	Met	Leu	Gln	Leu	Leu	Arg	Glu	Gln																																							
			260						265						270																																							
Phe	Pro	Glu	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala	Thr																																							
			275				280						285																																									
Ser	Ile	Gly	Lys	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu																																							
			290				295					300																																										
Asp	Ile	Gly	Thr	Ile	Ala	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	Thr																																							
			305			310				315				320																																								
Lys	Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Phe	Ala	Pro	Ile																																							
				325					330					335																																								
Tyr	Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala	Asp																																							
			340					345					350																																									
Val	Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	Lys	Asn	Cys	Lys																																							
			355				360					365																																										
Ile	Asn	His	Ser	Val	Val	Gly	Leu	Arg	Ser	Cys	Ile	Ser	Glu	Gly	Ala																																							
			370			375					380																																											
Ile	Ile	Glu	Asp	Ser	Leu	Leu	Met	Gly	Ala	Asp	Tyr	Tyr	Glu	Thr	Glu																																							
			385			390				395				400																																								
Ala	Asp	Lys	Lys	Leu	Leu	Ala	Glu	Lys	Gly	Gly	Ile	Pro	Ile	Gly	Ile																																							
				405					410					415																																								
Gly	Lys	Asn	Ser	Cys	Ile	Arg	Arg	Ala	Ile	Ile	Asp	Lys	Asn	Ala	Arg																																							
				420				425				430																																										
Ile	Gly	Asp	Asn	Val	Lys	Ile	Leu	Asn	Ala	Asp	Asn	Val	Gln	Glu	Ala																																							
			435				440					445																																										
Ala	Met	Glu	Thr	Asp	Gly	Tyr	Phe	Ile	Lys	Gly	Gly	Ile	Val	Thr	Val																																							
			450			455					460																																											
Ile	Lys	Asp	Ala	Leu	Leu	Pro	Ser	Gly	Thr	Val	Ile																																											
			465			470				475																																												

&lt;210&gt; 11

&lt;211&gt; 1582

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (10)..(1563)

&lt;223&gt; Shrunk-2 gene revertant form

&lt;220&gt;

&lt;221&gt; variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 11

```

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
      Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1             5             10

```

```

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

```

```

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

```

```

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50             55             60

```

```

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65             70             75

```

```

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
      80             85             90

```

```

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
      95             100             105             110

```

```

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
          115             120             125

```

```

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
          130             135             140

```

```

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
          145             150             155

```

```

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
          160             165             170

```

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579  
 Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe  
 175 180 185 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627  
 Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile  
 195 200 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675  
 Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu  
 210 215 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct 723  
 Val Gln Lys His Val Glu Asp Ala Asp Ile Thr Ile Ser Cys Ala  
 225 230 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat 771  
 Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp  
 240 245 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat 819  
 His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp  
 255 260 265 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat 867  
 Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp  
 275 280 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc 915  
 Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe  
 290 295 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta 963  
 Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu  
 305 310 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cat agt 1011  
 His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser  
 320 325 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059  
 Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile  
 335 340 345 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107  
 Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys  
 355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys  
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203  
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile  
 385 390 395



```

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                405                410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                420                425                430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
    435                440                445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
    450                455                460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
    465                470                475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                485                490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539
Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
495                500                505                510

acc atc aac gat ggg tct gtc ata tagatcggt cggtktgctg 1582
Thr Ile Asn Asp Gly Ser Val Ile
    515

```

<210> 12  
 <211> 518  
 <212> PRT  
 <213> Zea mays

<400> 12

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1                5                10                15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
    20                25                30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
    35                40                45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                55                60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
    65                70                75                80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
    85                90                95

```

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400

```

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
      405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
      420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
      435                      440                      445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
      450                      455                      460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
      465                      470                      475                      480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
      485                      490                      495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
      500                      505                      510

Asn Asp Gly Ser Val Ile
      515

```

```

<210> 13
<211> 1582
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

```

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<400> 13
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
      1              5              10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
      15              20              25              30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
      35              40              45

ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
      50              55              60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
      65              70              75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
      80              85              90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
      95              100              105              110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
      115              120              125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
      130              135              140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
      145              150              155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
      160              165              170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
      175              180              185              190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
      195              200              205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
      210              215              220

```

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460  
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475  
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490  
 tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539  
 Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala  
 495 500 505 510  
 acc atc aac gat ggg tct gtc ata tagatcggct gcgctktgcg 1582  
 Thr Ile Asn Asp Gly Ser Val Ile  
 515

<210> 14  
 <211> 518  
 <212> PRT  
 <213> Zea mays

<400> 14

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala

145	150	155	160
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro	165	170	175
Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp	180	185	190
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile	195	200	205
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln	210	215	220
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val	225	230	240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr	245	250	255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn	260	265	270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala	275	280	285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys	290	295	300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp	305	310	320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln	325	330	335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser	340	345	350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp	355	360	365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro	370	375	380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp	385	390	395
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val	405	410	415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met	420	425	430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu	435	440	445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn			

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      450              455              460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465              470              475              480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
      485              490              495
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
      500              505              510
Asn Asp Gly Ser Val Ile
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<210> 15
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

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      1              5              10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
      15              20              25              30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

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35										40										45										
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct	195																													
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala																														
50	55	60																												
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat	243																													
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr																														
65	70	75																												
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291																													
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly																														
80	85	90																												
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339																													
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro																														
95	100	105	110																											
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387																													
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe																														
115	120	125																												
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435																													
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr																														
130	135	140																												
tgc ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483																													
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn																														
145	150	155																												
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531																													
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu																														
160	165	170																												
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579																													
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe																														
175	180	185	190																											
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627																													
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile																														
195	200	205																												
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675																													
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu																														
210	215	220																												
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723																													
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala																														
225	230	235																												
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771																													
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp																														
240	245	250																												
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819																													
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp																														

255	260	265	270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat				867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc				915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta				963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	305	310	315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt				1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc				1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	335	340	345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag				1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	355	360	365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc				1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	370	375	380	
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Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att				1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg				1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta				1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata				1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg				1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg				1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	480	485	490	

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 16  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 16

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln

210	215	220
Lys His Val Glu Asp	Asp Ala Asp Ile Thr	Ile Ser Cys Ala Pro Val
225	230	235 240
Asp Glu Ser Arg Ala	Ser Lys Asn Gly Leu	Val Lys Ile Asp His Thr
	245	250 255
Gly Arg Val Leu Gln Phe	Phe Glu Lys Pro Lys Gly	Ala Asp Leu Asn
	260	265 270
Ser Met Arg Val Glu Thr	Asn Phe Leu Ser Tyr Ala	Ile Asp Asp Ala
	275	280 285
Gln Lys Tyr Pro Tyr Leu	Ala Ser Met Gly Ile Tyr	Val Phe Lys Lys
	290	295 300
Asp Ala Leu Leu Asp	Leu Leu Lys Ser Lys	Tyr Thr Gln Leu His Asp
305	310	315 320
Phe Gly Ser Glu Ile Leu	Pro Arg Ala Val Leu	Asp Tyr Ser Val Gln
	325	330 335
Ala Cys Ile Phe Thr Gly	Tyr Trp Glu Asp Val	Gly Thr Ile Lys Ser
	340	345 350
Phe Phe Asp Ala Asn Leu	Ala Leu Thr Glu Gln Pro	Ser Lys Phe Asp
	355	360 365
Phe Tyr Asp Pro Lys Thr	Pro Phe Phe Thr Ala	Pro Arg Cys Leu Pro
	370	375 380
Pro Thr Gln Leu Asp Lys	Cys Lys Met Lys Tyr Ala	Phe Ile Ser Asp
385	390	395 400
Gly Cys Leu Leu Arg	Glu Cys Asn Ile Glu	His Ser Val Ile Gly Val
	405	410 415
Cys Ser Arg Val Ser Ser	Gly Cys Glu Leu Lys	Asp Ser Val Met Met
	420	425 430
Gly Ala Asp Ile Tyr Glu	Thr Glu Glu Glu Ala Ser	Lys Leu Leu Leu
	435	440 445
Ala Gly Lys Val Pro Val	Gly Ile Gly Arg Asn Thr	Lys Ile Arg Asn
	450	455 460
Cys Ile Ile Asp Met Asn	Ala Arg Ile Gly Lys	Asn Val Val Ile Thr
465	470	475 480
Asn Ser Lys Gly Ile Gln	Glu Ala Asp His Pro	Glu Glu Gly Tyr Tyr
	485	490 495
Ile Arg Ser Gly Ile Val	Val Ile Leu Lys	Asn Ala Thr Ile Asn Asp
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Gly Ser Val Ile		

515

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<210> 17
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

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          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
           35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
           50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

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Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly		
	80					85					90						
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339	
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	110	
	95				100				105								
gtt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387	
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe		
				115					120					125			
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435	
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr		
			130					135					140				
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483	
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
		145					150					155					
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531	
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160				165						170						
gag	cca	ccn	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Pro	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
	175				180				185						190		
atc	tggt	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
				195				200						205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
				210				215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225				230						235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
	240				245					250							
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
	255				260				265					270			
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275				280						285			

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	
480 485 490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc	1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile	
495 500 505 510	

aac gat ggg tct gtc ata tagatcggct gcgktktgcg  
 Asn Asp Gly Ser Val Ile  
 515

1576

<210> 18  
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 <212> PRT  
 <213> Zea mays

<400> 18

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 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
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 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
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<210> 19  
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<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
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<222> (1008)
<223> y = c or t.

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<223> r = a or g; amino acid 453 = Pro.

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<223> h = a or c or t/u.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
      35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
      50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

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65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291		
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly			
80 85 90			
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339		
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro			
95 100 105 110			
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387		
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe			
115 120 125			
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435		
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr			
130 135 140			
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483		
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
145 150 155			
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531		
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
160 165 170			
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579		
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175 180 185 190			
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Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
195 200 205			
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675		
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
210 215 220			
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Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
225 230 235			
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771		
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
240 245 250			
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His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255 260 265 270			
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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275 280 285			
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915		

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Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	
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His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	
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gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	
335					340					345				350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	
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ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	
			370					375					380			
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Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	
		385				390						395				
tca	cay	ggt	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att	1251
Ser	His	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	
		400				405					410					
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg	1299
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	
415					420					425				430		
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Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	
				435					440					445		
ctg	tta	gct	ggg	aag	gtc	ccr	ath	gga	ata	gga	agg	aac	aca	aag	ata	1395
Leu	Leu	Ala	Gly	Lys	Val	Pro	Ile	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile	
			450					455					460			
agg	aac	tgt	atc	att	gac	atg	aat	gct	agg	att	ggg	aag	aac	gtg	gtg	1443
Arg	Asn	Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	
		465					470					475				
atc	aca	aac	agt	aag	ggc	atc	caa	gag	gct	gat	cac	ccg	gaa	gaa	ggg	1491
Ile	Thr	Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly	
		480				485					490					
tac	tac	ata	agg	tct	gga	atc	gtg	gtg	atc	ctg	aag	aat	gca	acc	atc	1539
Tyr	Tyr	Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile	
495					500					505				510		
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<213> Zea mays

<400> 20

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          20              25              30

Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
          35              40              45

Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
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Glu  Thr  Leu  His  Ser  Gln  Thr  Gln  Ser  Ser  Arg  Lys  Asn  Tyr  Ala  Asp
   65              70              75              80

Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Thr  Gly  Ser  Gln
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Leu  Phe  Pro  Leu  Thr  Ser  Thr  Arg  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
          100             105             110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
          115             120             125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
          130             135             140

Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Ile  Asn  Phe  Ala
   145             150             155             160

Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
          165             170             175

Ala  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
          180             185             190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
          195             200             205

Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
          210             215             220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
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Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
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Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp				
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Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser				
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Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro				
	370				375						380								
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	His				
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Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	Gly	Val				
			405					410						415					
Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	Met	Met				
		420						425					430						
Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	Leu	Leu				
	435				440							445							
Ala	Gly	Lys	Val	Pro	Ile	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile	Arg	Asn				
	450				455						460								
Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	Ile	Thr				
465					470				475					480					
Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly	Tyr	Tyr				
			485					490						495					
Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile	Asn	Asp				
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&lt;210&gt; 21

&lt;211&gt; 1576

&lt;212&gt; DNA

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<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (321)
<223> n = a or g or c or t/u, unknown, or other.

<220>
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<222> (1008)
<223> y = c or t.

<220>
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<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
      50             55             60

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Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
      65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly

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Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro			
95	100	105	110
ggt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc			387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe			
	115	120	125
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act			435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr			
	130	135	140
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac			483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
	145	150	155
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa			531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
	160	165	170
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt			579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
	175	180	185
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
	195	200	205
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
	210	215	220
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
	225	230	235
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
	240	245	250
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
	255	260	265
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
	275	280	285
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
	290	295	300
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
	305	310	315



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335 340 345 350	
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Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
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435 440 445	
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Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	
480 485 490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc	1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile	
495 500 505 510	
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Asn Asp Gly Ser Val Ile	
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&lt;213&gt; Zea mays

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Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
          35              40              45

Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
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Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Thr  Gly  Ser  Gln
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Leu  Phe  Pro  Leu  Thr  Ser  Thr  Thr  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
          100              105              110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
          115              120              125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
          130              135              140

Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Ile  Asn  Phe  Ala
  145              150              155              160

Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
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Ala  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
          180              185              190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
          195              200              205

Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
          210              215              220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
  225              230              235              240

Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
          245              250              255

Gly  Arg  Val  Leu  Gln  Phe  Phe  Glu  Lys  Pro  Lys  Gly  Ala  Asp  Leu  Asn
          260              265              270

Ser  Met  Arg  Val  Glu  Thr  Asn  Phe  Leu  Ser  Tyr  Ala  Ile  Asp  Asp  Ala
          275              280              285

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Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495  
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510  
 Gly Ser Val Ile  
 515

<210> 23

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
 heat stable

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<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1389)
<223> h = a or c or t/u.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

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        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
      35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
  50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
  65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly
  80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
  95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

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115										120										125									
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act					435									
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr														
				130				135					140																
tgc	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac					483									
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn														
				145				150					155																
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	oct	gaa					531									
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu														
				160				165					170																
gag	cca	gct	gga	tggt	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt					579									
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe														
				175				180					185			190													
atc	tggt	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att					627									
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile														
				195						200				205															
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt					675									
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu														
				210				215					220																
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct					723									
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala														
				225				230					235																
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat					771									
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp														
				240				245					250																
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat					819									
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp														
				255				260					265			270													
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat					867									
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp														
				275						280				285															
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc					915									
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe														
				290				295					300																
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta					963									
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu														
				305				310					315																
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt					1011									
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser														
				320				325					330																
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tggt	gag	gat	gtt	gga	aca	atc					1059									
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile														
				335				340					345			350													

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aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile
450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495 500 505 510

aac gat ggg tct gtc ata tagatcggtc gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
515

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&lt;210&gt; 24

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 24

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1 5 10 15

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile

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20					25					30					
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly
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Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
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Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
	65					70					75				80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Gly	Thr	Gly	Gln
			85						90					95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100					105					110		
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
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Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
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	145					150					155				160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
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Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
		180						185					190		
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
	210					215					220				
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
	225					230					235				240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
			245						250					255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260					265					270		
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
		275					280					285			
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
	290					295					300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
	305					310					315				320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	Val	Gln

325										330										335																																			
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser																																								
					340																				345																														
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp																																								
			355						360																																														
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro																																								
			370						375																																														
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	Asp																																								
			385						390																																														
Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	Gly	Val																																								
					405																																																		
Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	Met	Met																																								
					420																																																		
Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	Leu	Leu																																								
					435																																																		
Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Ile	Lys	Ile	Arg	Asn																																								
					450																																																		
Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	Ile	Thr																																								
					470																																																		
Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly	Tyr	Tyr																																								
					485																																																		
Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile	Asn	Asp																																								
					500																																																		
Gly	Ser	Val	Ile																																																				
					515																																																		

<210> 25  
 <211> 1576  
 <212> DNA  
 <213> Zea mays  
  
 <220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunk-2 gene revertant form, modified to be  
 heat stable  
  
 <220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.  
  
 <220>  
 <221> variation



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<222> (657)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

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        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
      35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
      50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
      65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
      80             85             90

tct cag etc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
      95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
      115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
      130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn

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145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa			531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt			579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
195	200	205	
gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu			
210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
305	310	315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt			1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser			
320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
335	340	345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag			1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys			
355	360	365	
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Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			

370										375										380										
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Leu Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile																														
385	390	395																												
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251																													
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile																														
400	405	410																												
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299																													
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val																														
415	420	425	430																											
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347																													
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu																														
435	440	445																												
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395																													
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile																														
450	455	460																												
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443																													
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val																														
465	470	475																												
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491																													
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly																														
480	485	490																												
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc	1539																													
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile																														
495	500	505	510																											
aac gat ggg tct gtc ata tagatcggct gcgktg	1576																													
Asn Asp Gly Ser Val Ile																														
515																														

&lt;210&gt; 26

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 26

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile			
1	5	10	15
Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile			
20	25	30	
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly			
35	40	45	
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro			
50	55	60	

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365

```

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
  370                               375                   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                               390                   395                   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                               405                   410                   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                               420                   425                   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
  435                               440                   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
  450                               455                   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                               470                   475                   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
  485                               490                   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
  500                               505                   510

Gly Ser Val Ile
  515

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<210> 27
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

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<220>  
 <221> variation  
 <222> (1287)  
 <223> y = c or t.

<220>  
 <221> variation

<222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1578)  
 <223> k = g or t.

<400> 27  
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
           Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
           1                                  5                                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
   15                                  20                                  25                                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                                   35                                  40                                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                                   50                                  55                                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                                   65                                  70                                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
   80                                  85                                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
   95                                  100                                  105                                  110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
                                   115                                  120                                  125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
                                   130                                  135                                  140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn  
   145                                  150                                  155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	

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ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
      385              390              395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
      400              405              410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val
      415              420              425              430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
              435              440              445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
              450              455              460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
      465              470              475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480              485              490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
      495              500              505              510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
      515

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&lt;210&gt; 28

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 28

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1              5              10              15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
      20              25              30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
      50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp

```



65	70	75	80
Ala Asn Arg Val Ser	Ala Ile Ile Leu	Gly Gly Thr Gly Ser Gln	
85		90	95
Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly			
100	105		110
Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser			
115	120		125
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu			
130	135		140
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn Phe Ala			
145	150	155	160
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro			
165	170		175
Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp			
180	185		190
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile			
195	200		205
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln			
210	215	220	
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val			
225	230	235	240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr			
245	250		255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn			
260	265		270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala			
275	280		285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys			
290	295	300	
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp			
305	310	315	320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln			
325	330		335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser			
340	345		350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp			
355	360		365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro			

```

370          375          380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385          390          395          400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
405          410          415
Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met
420          425          430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
435          440          445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
450          455          460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465          470          475          480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
485          490          495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
500          505          510
Gly Ser Val Ile
515

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```

<210> 29
<211> 1576
<212> DNA
<213> Zea mays

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<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

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<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

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<220>
<221> variation
<222> (981)
<223> r = g or a.

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<220>
<221> variation
<222> (1008)
<223> y = c or t.

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<220>

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<221> variation
<222> (1086)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 29
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
      Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly
      80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
      95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
        115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
        130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

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Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
		145					150					155					
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531	
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160					165					170						
gag	cca	gct	gga	tggttc	cag	gggt	aca	gca	gac	tct	atc	aga	aaa	ttt		579	
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
	175					180					185				190		
atc	tggt	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
					195				200					205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cggt	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
		240				245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	gggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
	255				260				265					270			
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
			275					280						285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915	
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu		
		305				310						315					
cat	gac	ttt	gga	tct	aar	atc	ctc	cca	aga	gct	gta	cta	gat	cay	agt	1011	
His	Asp	Phe	Gly	Ser	Lys	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser		
		320				325					330						
gtg	cag	gca	tgct	att	ttt	acg	ggc	tat	tggt	gag	gat	gtt	gga	aca	atc	1059	
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile		
	335				340				345					350			
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gtt	ctc	act	gag	cag	cct	tcc	aag	1107	
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Val	Leu	Thr	Glu	Gln	Pro	Ser	Lys		
				355			360						365				
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155	
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys		

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370          375          380
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
385          390          395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400          405          410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415          420          425          430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435          440          445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
450          455          460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
465          470          475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480          485          490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495          500          505          510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
515

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<210> 30
<211> 516
<212> PRT
<213> Zea mays

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<400> 30

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1          5          10          15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
20          25          30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
35          40          45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
50          55          60

```

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365

```

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
  370                               375                               380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385                               390                               395                               400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                               405                               410                               415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                               420                               425                               430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
  435                               440                               445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
  450                               455                               460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                               470                               475                               480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                               485                               490                               495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
  500                               505                               510

Gly Ser Val Ile
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<210> 31
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

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<220>
<221> variation
<222> (1578)
<223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15              20              25              30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
              35              40              45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
              50              55              60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
              65              70              75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
80              85              90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95              100              105              110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
              115              120              125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
              130              135              140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Leu Glu Gly Gly Ile Asn
145              150              155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
160              165              170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175              180              185              190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile

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195										200										205									
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Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu														
				210					215					220															
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct					723									
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala														
				225				230																					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat					771									
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp														
				240				245																					
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggg	gct	gat					819									
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp														
				255			260				265				270														
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Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp														
				275				280							285														
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc					915									
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe														
				290				295						300															
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta					963									
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu														
				305				310						315															
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tty	agt					1011									
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Phe	Ser														
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gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc					1059									
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile														
				335			340					345			350														
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag					1107									
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys														
				355				360						365															
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc					1155									
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys														
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Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile														
				385				390						395															
tca	gat	ggg	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att					1251									
Ser	Asp	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile														
				400				405						410															
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg					1299									
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val														
				415				420						425															

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu  
                   435                  440                  445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
                   450                  455                  460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
                   465                  470                  475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
                   480                  485                  490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
                   495                  500                  505                  510

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<210> 32

<211> 516

<212> PRT

<213> Zea mays

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                   20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
                   35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
                   50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
   65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
                   85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
                   100                  105                  110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
                   115                  120                  125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
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 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
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Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
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Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510

Gly Ser Val Ile  
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<210> 33

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 33

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15	20	25	30	
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt				147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe	35	40	45	
ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct				195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	50	55	60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat				243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga				291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly	80	85	90	
tct cag etc ttt cct ctg aca agc aca aga gct acg cct gct gta cct				339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	95	100	105	110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc				387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	115	120	125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act				435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac				483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa				531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt				579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att				627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt				675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct				723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat				771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	240	245	250	

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser	
320 325 330	
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Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
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Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	

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 ile thr asn ser lys gly ile gln glu ala asp his pro glu glu gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 tyr tyr ile arg ser gly ile val val ile leu lys asn ala thr ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktkgc 1576  
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 515

<210> 34

<211> 516

<212> PRT

<213> Zea mays

<400> 34

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile

195				200				205							
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
210						215					220				
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
225					230					235				240	
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
				245					250					255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260						265					270	
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
			275						280					285	
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
			290			295					300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
305					310					315					320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Met	Ser	Val	Gln
				325					330					335	
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
			340						345					350	
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp
			355				360							365	
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro
			370			375					380				
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	Asp
385					390					395					400
Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	Gly	Val
				405					410					415	
Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	Met	Met
			420						425					430	
Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	Leu	Leu
			435				440							445	
Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile	Arg	Asn
			450			455					460				
Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	Ile	Thr
465					470					475				480	
Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly	Tyr	Tyr
				485					490					495	
Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile	Asn	Asp



500

505

510

Gly Ser Val Ile  
515

&lt;210&gt; 35

&lt;211&gt; 1576

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
heat stable

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (267)

&lt;223&gt; k = g or t; amino acid 86 = Ala.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (540)

&lt;223&gt; n = a or g or c or t/u, unknown, or other.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1008)

&lt;223&gt; y = c or t.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1368)

&lt;223&gt; r = a or g; amino acid 453 = Pro.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1578)

&lt;223&gt; k = g or t.

&lt;400&gt; 35

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1

5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50	55	60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr 65 70 75			243
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly 80 85 90			291
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro 95 100 105 110			339
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe 115 120 125			387
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr 130 135 140			435
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn 145 150 155			483
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu 160 165 170			531
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190			579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205			627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220			675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235			723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250			771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270			819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			867

275										280										285									
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc					915									
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe														
			290						295					300															
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta					963									
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu														
			305					310					315																
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt					1011									
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser														
			320			325					330																		
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc					1059									
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile														
			335			340				345				350															
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag					1107									
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys														
					355				360					365															
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc					1155									
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys														
				370				375					380																
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc					1203									
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile														
				385				390					395																
tca	gat	ggt	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att					1251									
Ser	Asp	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile														
				400			405					410																	
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg					1299									
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val														
				415		420				425				430															
atg	atg	gga	gcy	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta					1347									
Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu														
					435				440				445																
ctg	tta	gct	ggg	aag	gtc	ccr	gtt	gga	ata	gga	agg	aac	aca	aag	ata					1395									
Leu	Leu	Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile														
					450				455				460																
agg	aac	tgt	atc	att	gac	atg	aat	gct	agg	att	ggg	aag	aac	gtg	gtg					1443									
Arg	Asn	Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val														
					465			470					475																
atc	aca	aac	agt	aag	ggc	atc	caa	gag	gct	gat	cac	ccg	gaa	gaa	ggg					1491									
Ile	Thr	Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly														
					480			485					490																
tac	tac	ata	agg	tct	gga	atc	gtg	gtg	atc	ctg	aag	aat	gca	acc	atc					1539									
Tyr	Tyr	Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile														
					500					505				510															

aac gat ggg tct gtc ata tagatcgggt gcgktktcgc  
 Asn Asp Gly Ser Val Ile  
 515

1576

<210> 36  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 36

Met	Gln	Phe	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Ser	Gly	Pro	His	Gln	Ile
1				5					10					15	
Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	Ser	Ile
			20					25					30		
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly
			35				40					45			
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
	50					55					60				
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
	65				70					75					80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
			85						90					95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100					105					110		
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
		115					120					125			
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
	130					135					140				
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
	145				150					155					160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
			165						170					175	
Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
			180					185					190		
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
	210					215					220				
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
	225				230					235					240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495  
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510  
 Gly Ser Val Ile  
 515

&lt;210&gt; 37

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<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 37
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
      Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
      35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
      50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
      65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

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Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly		
80						85					90						
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339	
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro		
95					100					105					110		
ggt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387	
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe		
				115					120					125			
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435	
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr		
			130					135					140				
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483	
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
			145					150					155				
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531	
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
			160				165						170				
gag	cca	gct	gga	tggt	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
					180					185					190		
atc	tggt	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
				195					200					205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
				210				215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
			225				230						235				
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
			240			245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
				255		260				265				270			
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275				280						285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915	
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	

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Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
   305                               310                               315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
   320                               325                               330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
   335                               340                               345                               350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
   355                               360                               365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
   370                               375                               380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
   385                               390                               395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
   400                               405                               410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
   415                               420                               425                               430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
   435                               440                               445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
   450                               455                               460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
   465                               470                               475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
   480                               485                               490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
   495                               500                               505                               510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg   1576
Asn Asp Gly Ser Val Ile
   515

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&lt;210&gt; 38



<211> 516  
 <212> PRT  
 <213> Zea mays

<400> 38

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Met  Gln  Phe  Ala  Leu  Ala  Leu  Asp  Thr  Asn  Ser  Gly  Pro  His  Gln  Ile
   1              5              10              15

Arg  Ser  Cys  Glu  Gly  Asp  Gly  Ile  Asp  Arg  Leu  Glu  Lys  Leu  Ser  Ile
          20              25              30

Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
          35              40              45

Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
   50              55              60

Glu  Thr  Leu  His  Ser  Gln  Thr  Gln  Ser  Ser  Arg  Lys  Asn  Tyr  Ala  Asp
   65              70              75              80

Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Thr  Gly  Ser  Gln
          85              90              95

Leu  Phe  Pro  Leu  Thr  Ser  Thr  Arg  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
          100             105             110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
          115             120             125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
          130             135             140

Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Ile  Asn  Phe  Ala
  145             150             155             160

Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
          165             170             175

Ala  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
          180             185             190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
          195             200             205

Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
          210             215             220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
  225             230             235             240

Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
          245             250             255

Gly  Arg  Val  Leu  Gln  Phe  Phe  Glu  Lys  Pro  Lys  Gly  Ala  Asp  Leu  Asn
          260             265             270

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Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
    275                      280                      285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                      295                      300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
    305                      310                      315                      320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
    325                      330                      335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
    340                      345                      350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
    355                      360                      365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                      375                      380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
    385                      390                      395                      400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
    405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
    420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
    435                      440                      445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                      455                      460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
    465                      470                      475                      480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
    485                      490                      495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
    500                      505                      510

Gly Ser Val Ile
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<210> 39
<211> 1576
<212> DNA
<213> Zea mays

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<220>
<221> CDS
<222> (10)..(1563)

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<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1197)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 39

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           Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
             1             5             10
```

```
cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15             20             25             30
```

```
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
             35             40             45
```

```
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50             55             60
```

```
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
             65             70             75
```

```
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
             80             85             90
```

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95 100 105 110	
ggt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	

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cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt 1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
320 325 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335 340 345 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495 500 505 510

aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
515

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<210> 40
<211> 516
<212> PRT
<213> Zea mays

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&lt;400&gt; 40

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Arg  Ser  Cys  Glu  Gly  Asp  Gly  Ile  Asp  Arg  Leu  Glu  Lys  Leu  Ser  Ile
          20              25              30

Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
          35              40              45

Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
          50              55              60

Glu  Thr  Leu  His  Ser  Gln  Thr  Gln  Ser  Ser  Arg  Lys  Asn  Tyr  Ala  Asp
  65              70              75              80

Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Gly  Thr  Gly  Ser  Gln
          85              90              95

Leu  Phe  Pro  Leu  Thr  Ser  Thr  Arg  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
          100             105             110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
          115             120             125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
          130             135             140

Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Gly  Ile  Asn  Phe  Ala
  145             150             155             160

Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
          165             170             175

Val  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
          180             185             190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
          195             200             205

Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
          210             215             220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
  225             230             235             240

Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
          245             250             255

Gly  Arg  Val  Leu  Gln  Phe  Phe  Glu  Lys  Pro  Lys  Gly  Ala  Asp  Leu  Asn
          260             265             270

Ser  Met  Arg  Val  Glu  Thr  Asn  Phe  Leu  Ser  Tyr  Ala  Ile  Asp  Asp  Ala
          275             280             285

Gln  Lys  Tyr  Pro  Tyr  Leu  Ala  Ser  Met  Gly  Ile  Tyr  Val  Phe  Lys  Lys

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290	295	300
Asp Ala Leu Leu Asp	Leu Leu Lys Ser Lys Tyr Thr	Gln Leu His Asp
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Phe Gly Ser Glu Ile	Leu Pro Arg Ala Val	Leu Asp His Ser Val Gln
	325	330 335
Ala Cys Ile Phe Thr	Gly Tyr Trp Glu Asp Val	Gly Thr Ile Lys Ser
	340	345 350
Phe Phe Asp Ala Asn	Leu Ala Leu Thr Glu Gln	Pro Ser Lys Phe Asp
	355	360 365
Phe Tyr Asp Pro Lys	Thr Pro Phe Phe Thr	Ala Pro Arg Cys Leu Pro
	370	375 380
Pro Thr Gln Leu Asp	Lys Cys Lys Met Lys Tyr	Val Phe Ile Ser Asp
	385	390 395 400
Gly Cys Leu Leu Arg	Glu Cys Asn Ile Glu His	Ser Val Ile Gly Val
	405	410 415
Cys Ser Arg Val Ser	Ser Gly Cys Glu Leu Lys	Asp Ser Val Met Met
	420	425 430
Gly Ala Asp Ile Tyr	Glu Thr Glu Glu Glu Ala	Ser Lys Leu Leu Leu
	435	440 445
Ala Gly Lys Val Pro	Val Gly Ile Gly Arg Asn	Thr Lys Ile Arg Asn
	450	455 460
Cys Ile Ile Asp Met	Asn Ala Arg Ile Gly Lys	Asn Val Val Ile Thr
	465	470 475 480
Asn Ser Lys Gly Ile	Gln Glu Ala Asp His	Pro Glu Glu Gly Tyr Tyr
	485	490 495
Ile Arg Ser Gly Ile	Val Val Ile Leu Lys	Asn Ala Thr Ile Asn Asp
	500	505 510
Gly Ser Val Ile		
	515	

&lt;210&gt; 41

&lt;211&gt; 1576

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
heat stable

&lt;220&gt;

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gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	

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gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335 340 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415 420 425

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
450 455 460

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Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495 500 505 510

aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
515

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&lt;210&gt; 42

&lt;211&gt; 516

&lt;212&gt; FRT

&lt;213&gt; Zea mays

&lt;400&gt; 42

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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 20 25 30  
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300

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Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                      310                      315                      320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                      325                      330                      335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                      340                      345                      350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
355                      360                      365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
370                      375                      380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385                      390                      395                      400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                      405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
435                      440                      445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
450                      455                      460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                      470                      475                      480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
485                      490                      495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
500                      505                      510

Gly Ser Val Ile
515

```